RAW SEQUENCE LISTING DATE 04/09/2002
PATENT APPLICATION: **US/10/044,539** TIME: 11:38:58

Input Set : **N:\Crf3\RULE60\10044539.raw**
Output Set: **N:\CRF3\04092002\J044539.raw**

SEQUENCE LISTING

```
  3 (1) GENERAL INFORMATION:
  5       (i) APPLICANT: Cech, Thomas R.
  6                      Lingner, Joachim
  7                      Nakamura, Toru
  8                      Chapman, Karen B.
  9                      Morin, Gregg B.
 10                      Harley, Calvin
 11                      Andrews, William H.
 13     (ii) TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 14                              THERAPEUTIC METHODS
 16    (iii) NUMBER OF SEQUENCES: 335
 18     (iv) CORRESPONDENCE ADDRESS:
 19          (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 20          (B) STREET: Two Embarcadero Center, 8th Floor
 21          (C) CITY: San Francisco
 22          (D) STATE: California
 23          (E) COUNTRY: United States of America
 24          (F) ZIP: 94111
 26      (v) COMPUTER READABLE FORM:
 27          (A) MEDIUM TYPE: Floppy disk
 28          (B) COMPUTER: IBM PC compatible
 29          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 30          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 32     (vi) CURRENT APPLICATION DATA:
 33          (A) APPLICATION NUMBER: US/10/044,539
 34          (B) FILING DATE: 11-Jan-2002
 66          (C) CLASSIFICATION: 435
 63    (vii) PRIOR APPLICATION DATA:
 39          (A) APPLICATION NUMBER: 08/912,951
 40          (B) FILING DATE:
 44          (A) APPLICATION NUMBER: US 08/854,050
 45          (B) FILING DATE: 09-MAY-1997
 49          (A) APPLICATION NUMBER: US 08/851,843
 50          (B) FILING DATE: 06-MAY-1997
 54          (A) APPLICATION NUMBER: US 08/846,017
 55          (B) FILING DATE: 25-APR-1997
 59          (A) APPLICATION NUMBER: US 08/844,419
 60          (B) FILING DATE: 18-APR-1997
 64          (A) APPLICATION NUMBER: US 08/724,643
 65          (B) FILING DATE: 01-OCT-1996
 68   (viii) ATTORNEY/AGENT INFORMATION:
 69          (A) NAME: Apple, Randolph T.
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C--> 33
C--> 34

ENTERED

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70              (B) REGISTRATION NUMBER: 36,429
71              (C) REFERENCE/DOCKET NUMBER: 015389-002600US
73      (ix) TELECOMMUNICATION INFORMATION:
74              (A) TELEPHONE: (415) 576-0200
75              (B) TELEFAX: (415) 576-0300
77 (2) INFORMATION FOR SEQ ID NO: 1:
79      (i) SEQUENCE CHARACTERISTICS:
80              (A) LENGTH: 4015 base pairs
81              (B) TYPE: nucleic acid
82              (C) STRANDEDNESS: single
83              (D) TOPOLOGY: linear
85      (ii) MOLECULE TYPE: cDNA
88      (ix) FEATURE:
89              (A) NAME/KEY: CDS
90              (B) LOCATION: 56..3454
91              (D) OTHER INFORMATION: /product= "hTRT"
92 /note= "human telomerase reverse
93 transcriptase (hTRT) catalytic protein
94 component"
97      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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100                                                                   Met
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103 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC       106
104 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
105             5                   10                  15
107 TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC       154
108 Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
109         20                  25                  30
111 CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG       202
112 Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala
113         35                  40                  45
115 CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC       250
116 Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro
117 50                  55                  60                  65
119 CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG       298
120 Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val
121                 70                  75                  80
123 GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG       346
124 Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu
125             85                  90                  95
127 GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG       394
128 Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu
129         100                 105                 110
131 GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC       442
132 Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp
133     115                 120                 125
135 GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC       490
136 Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly
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137 130                         135                 140                        145
139 GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG          538
140 Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu
141                         150                 155                 160
143 GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG          586
144 Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln
145                         165                 170                 175
147 CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC          634
148 Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro
149                 180                 185                 190
151 CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG          682
152 Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu
153         195                 200                 205
155 GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG          730
156 Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly
157 210                         215                 220                 225
159 GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC          778
160 Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly
161                 230                 235                 240
163 GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC          826
164 Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala
165                 245                 250                 255
167 CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG·GTG          874
168 His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val
169         260                 265                 270
171 TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC          922
172 Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu
173         275                 280                 285
175 TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG          970
176 Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala
177 290                         295                 300                 305
179 GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT          1018
180 Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys
181                 310                 315                 320
183 CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC          1066
184 Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp
185                 325                 330                 335
187 AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC          1114
188 Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser
189         340                 345                 350
191 CTG ACT GGC GCT CGG AGG CTC GTG·GAG ACC ATC TTT CTG GGT TCC AGG          1162
192 Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg
193         355                 360                 365
195 CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC          1210
196 Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg
197 370                         375                 380                 385
199 TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG          1258
200 Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala
201                 390                 395                 400
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Input Set : N:\Crf3\RULE60\10044539.raw
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203 CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT      1306
204 Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala
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207 GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC      1354
208 Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly
209             420             425             430
211 TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG      1402
212 Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val
213             435             440             445
215 CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG      1450
216 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val
217 450             455             460             465
219 CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG      1498
220 Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg
221             470             475             480
223 CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG      1546
224 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu
225             485             490             495
227 GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC      1594
228 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser
229             500             505             510
231 GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT      1642
232 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val
233             515             520             525
235 CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG      1690
236 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu
237 530             535             540             545
239 CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT      1738
240 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe
241             550             555             560
243 TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG      1786
244 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg
245             565             570             575
247 AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG      1834
248 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu
249             580             585             590
251 AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT      1882
252 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His
253             595             600             605
255 CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC      1930
256 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro
257 610             615             620             625
259 AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA      1978
260 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly
261             630             635             640
263 GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG      2026
264 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
265             645             650             655
267 GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC      2074
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268 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro
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272 Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala
273         675                 680                 685
275 TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG      2170
276 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu
277 690                 695                 700                 705
279 CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC      2218
280 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro
281                 710                 715                 720
283 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC      2266
284 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn
285                 725                 730                 735
287 ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG      2314
288 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly
289         740                 745                 750
291 CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC      2362
292 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu
293         755                 760                 765
295 CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG      2410
296 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro
297 770                 775                 780                 785
299 CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC      2458
300 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala
301         ·         790                 795                 800
303 AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC      2506
304 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala
305                 805                 810                 815
307 GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG      2554
308 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln
309         820                 825                 830
311 GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG      2602
312 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met
313         835                 840                 845
315 GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT      2650
316 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg
317 850                 855                 860                 865
319 TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA      2698
320 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys
321                 870                 875                 880
323 ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG      2746
324 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val
325         885                 890                 895
327 GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC      2794
328 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala
329         900                 905                 910
331 CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC      2842
332 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/044,539**

DATE: 04/09/2002
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Input Set : **N:\Crf3\RULE60\10044539.raw**
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L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
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L:2081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:4351 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=105
L:4373 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=106
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L:4424 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:4424 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=108
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L:5165 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 111
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